



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/825,561
Source: OIP
Date Processed by STIC: 5/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/825,561

DATE: 05/30/2001

TIME: 15:13:21

Input Set : A:\00-22.SEQ.txt

Output Set: C:\CRF3\05302001\I825561.raw

Does Not Comply
Corrected Diskette Needed
Pb

```

4 <110> APPLICANT: Sprecher, Cindy A.
5 Novak, Julia E.
6 West, James W.
7 Presnell, Scott R.
8 Holly, Richard D.
9 Nelson, Andrew J.
11 <120> TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
13 <130> FILE REFERENCE: 00-22
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/825,561
C--> 15 <141> CURRENT FILING DATE: 2001-04-03
15 <150> PRIOR APPLICATION NUMBER: US 60/194,731
16 <151> PRIOR FILING DATE: 2000-04-05
18 <150> PRIOR APPLICATION NUMBER: US 60/222,121
19 <151> PRIOR FILING DATE: 2000-07-28
21 <160> NUMBER OF SEQ ID NOS: 86
23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1614
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)...(1614)
34 <400> SEQUENCE: 1
35 atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga      88
36 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
37 1 5 10 15
39 ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg      96
40 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
41 20 25 30
43 gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc      144
44 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
45 35 40 45
47 ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc      192
48 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
49 50 55 60
51 tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc      240
52 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
53 65 70 75 80
55 tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc      288
56 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
57 85 90 95
59 aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt      336
60 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
61 100 105 110
63 ctc ctg gct gac agc atc aag ccg gct ccc cct ttc aac gtg act gtg      384
64 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val

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Input Set : A:\00-22.SEQ.txt

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65          115          120          125
67 acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac      432
68 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
69      130      135      140
71 cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac      480
72 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
73      145      150      155      160
75 agg aac cgg gga gac ccc tgg gct gtg agt ccc agg aga aag ctg atc      528
76 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
77      165      170      175
79 tca gtg gac tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa      576
80 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
81      180      185      190
83 gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc      624
84 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
85      195      200      205
87 tcc tac cag ggg acc tgg agt gaa tgg agt gac ccc gtc atc ttt cag      672
88 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
89      210      215      220
91 acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt      720
92 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
93      225      230      235      240
95 ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag      768
96 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
97      245      250      255
99 acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc      816
100 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
101      260      265      270
103 cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc      864
104 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
105      275      280      285
107 aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga      912
108 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
109      290      295      300
111 ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac      960
112 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
113      305      310      315      320
115 cca cca cgg agc cgg gcc aag agg ctg cag ctc acg gag cta caa gaa      1008
116 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Glu
117      325      330      335
119 cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg      1056
120 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Thr
121      340      345      350
123 ccg aca gcc cag aac tgg ggg gcc tca gct tac agt gag gag agg gat      1104
124 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
125      355      360      365
127 cgg cca tac gcc ctg gtg tcc att gac aca gtg act gtg cta gat gca      1152
128 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
129      370      375      380

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131 gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca      1200
132 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
133 385                               390                               395                               400
135 gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac      1248
136 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
137                               405                               410                               415
139 cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca      1296
140 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
141                               420                               425                               430
143 gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga      1344
144 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
145 435                               440                               445
147 cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc      1392
148 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
149 450                               455                               460
151 tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca      1440
152 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
153 465                               470                               475                               480
155 ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc      1488
156 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
157                               485                               490                               495
159 tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac      1536
160 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
161 500                               505                               510
163 gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg      1584
164 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
165 515                               520                               525
167 cca ctt tcg agc cct gga ccc cag gcc agc      1614
168 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
169 530                               535
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 538
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
177 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
178 1 5 10 15
179 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
180 20 25 30
181 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
182 35 40 45
183 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
184 50 55 60
185 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
186 65 70 75 80
187 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
188 85 90 95
189 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
190 100 105 110

```

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```

191 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
192      115      120      125
193 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
194      130      135      140
195 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
196 145      150      155      160
197 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
198      165      170      175
199 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
200      180      185      190
201 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
202      195      200      205
203 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
204      210      215      220
205 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
206 225      230      235      240
207 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
208      245      250      255
209 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
210      260      265      270
211 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
212      275      280      285
213 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
214      290      295      300
217 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
218 305      310      315      320
219 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
220      325      330      335
221 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
222      340      345      350
223 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
224      355      360      365
225 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
226      370      375      380
227 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
228 385      390      395      400
229 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
230      405      410      415
231 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
232      420      425      430
233 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
234      435      440      445
235 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
236      450      455      460
237 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
238 465      470      475      480
239 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
240      485      490      495
241 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp

```

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Output Set: C:\CRF3\05302001\I825561.raw

```

242          500          505          510
243 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
244          515          520          525
245 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
246          530          535
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 696
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)...(696)
257 <400> SEQUENCE: 3
258 ctg aac acg aca att ctg acg ccc aat ggg aat gaa gac acc aca gct      8
259 Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala
260 1 5 10 15
262 gat ttc ttc ctg acc act atg ccc act gac tcc ctc agt gtt tcc act      96
263 Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr
264 20 25 30
266 ctg ccc ctc cca gag gtt cag tgt ttt gtg ttc aat gtc gag tac atg      144
267 Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met
268 35 40 45
270 aat tgc act tgg aac agc agc tct gag ccc cag cct acc aac ctc act      192
271 Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
272 50 55 60
274 ctg cat tat tgg tac aag aac tcg gat aat gat aaa gtc cag aag tgc      240
275 Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
276 65 70 75 80
278 agc cac tat cta ttc tct gaa gaa atc act tct ggc tgt cag ttg caa      288
279 Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
280 85 90 95
282 aaa aag gag atc cac ctc tac caa aca ttt gtt gtt cag ctc cag gac      336
283 Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
284 100 105 110
286 cca cgg gaa ccc agg aga cag gcc aca cag atg cta aaa ctg cag aat      384
287 Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
288 115 120 125
290 ctg gtg atc ccc tgg gct cca gag aac cta aca ctt cac aaa ctg agt      432
291 Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
292 130 135 140
294 gaa tcc cag cta gaa ctg aac tgg aac aac aga ttc ttg aac cac tgt      480
295 Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
296 145 150 155 160
298 ttg gag cac ttg gtg cag tac cgg act gac tgg gac cac agc tgg act      528
299 Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
300 165 170 175
302 gaa caa tca gtg gat tat aga cat aag ttc tcc ttg cct agt gtg gat      576
303 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
304 180 185 190

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<210> 16
 <211> 567
 <212> PPT
 <213> Artificial Sequence

see item 11 on Enr Summary sheet

<400> 16
 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
 1 5 10 15

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/825,561

DATE: 05/30/2001
TIME: 15:13:22

Input Set : A:\00-22.SEQ.txt
Output Set : C:\CRF3\05302001\I825561.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1018 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1018 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1207 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1207 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1560 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1560 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1645 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1645 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67

VERIFICATION SUMMARY

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Input Set : A:\00-22.SEQ.txt

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L:2554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71

L:2556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71

L:2720 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:2720 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: